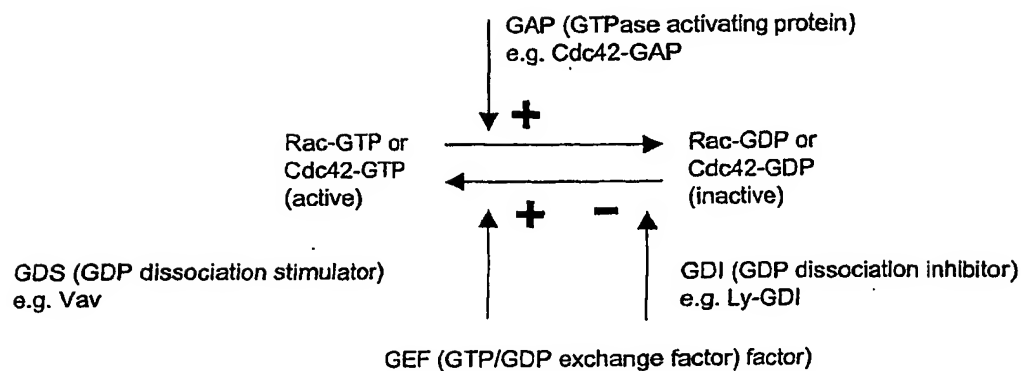


**Figure 1.**

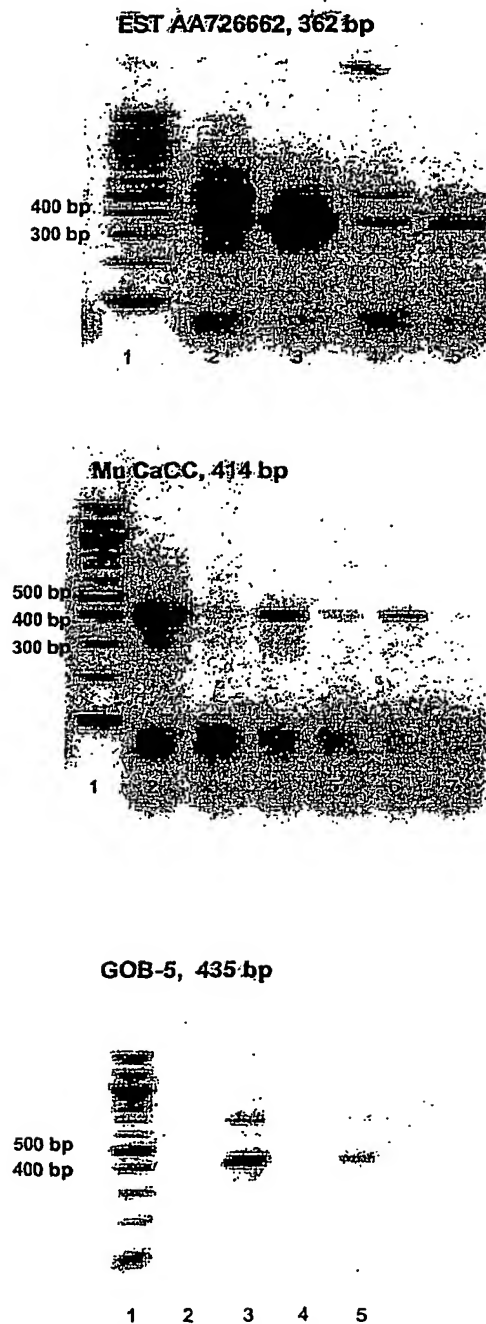


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Figure 2:



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Figure 3.  
IgE receptor.

CLUSTAL W (1.81) multiple sequence alignment

```
ige_r_beta_mouse  MDTENRSRADLALPNPQESSAPDIEELLEASP-----AKAAPPKQTWRTPLKKBL 50
ige_r_beta_human  MDTESNRRANLALP--QEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQ 58
lr8_mouse         MVQSTVTVNGVKVASTHPQSAHISIHQKSALEQLLG---AVGSLKKFLSWP-----Q 51
lr8_human         MTQNTVIVNGVAMASRHAQPTHVNVHMQESALTQLLK---AGGSLKKFLFHPGDTVSS 57
                  *  ..  .: .:  :  .:  .: .:  *  .:  :

ige_r_beta_mouse  EFLGATQILVGLICLCFGTIVCSVLYVSDPDEEVILLYKLGYPFWGAVLFVLSGFLSIIS 110
ige_r_beta_human  EFLGVTQILTAMICLCFGTVVCSVLDSHIEGDIFFSFRAGYPPFGAIFFSISGMLSIIIS 118
lr8_mouse         ARVHYGQLSLGVTQILLGLVSC-ALGVCLYFGPWTELCAFGCAFWSGSAVILAGVGTIVH 110
lr8_human         ARIGYEQLALGVTQILLGVVSC-VLGVCLSLGPWTVLRASGCAFWSGVVIAAGAGAIHV 116
                  :  *:  .:  :  *:  *  *  .:  *  .**..  :  *:  :

ige_r_beta_mouse  ERKNTLYLVRGSLGANIVSSIAAGTGIAMLIIN-----LT 145
ige_r_beta_human  ERRNATYLVRGSLGANTASSIAGGTGITILIIN-----LK 153
lr8_mouse         EKROGK-LSGQVSCLLLLACIATAAAATVLGVNSLIRQTSVPYYVEIFS-TCNPLQSSMD 168
lr8_human         EKHPGK-LAGYISSLLTLAGFATAMAADVLCVNSPINQTBPFYIDTVCDRSDPVFP--T 173
                  *::  *  .:  *:  .:  *:  :

ige_r_beta_mouse  NNFAYMN--NCKNVTEDDGCFFVASFTTELVLMMFLTLILAFCSAVLFTIYRIGQELESKK 203
ige_r_beta_human  KSLAYIHHSQCQFFETK-CFMASFSTEIVVMMLFLTILGLGSVSLTICGAGEELKGNK 212
lr8_mouse         PGYGTVRYSDSDWKTERCREYLNMMNLFALFCIMLTIVVCILEIVVSVASLGLSLRSMY 228
lr8_human         TGYRWMRRSQENQWQKEECRAYMQMLRKLFTAIRALFLAVCVLEKIVVSLVSLGVGLRNL 233
                  .  .:  .:  .:  .:  .:  .:  .:  .:  .:  *  *..

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ige_r_beta_human  VPEDRVYEELNIYSATYSELEDPGEMSPPIDL----- 244
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lr8_human         GQSSQPLNEEGSEKRLLGNSVPPSPSREQTSTAIVL 270
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**Figure 4**

**Sequence R1-OS-B1-E5:**

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**Sequence OtS2-C5:**

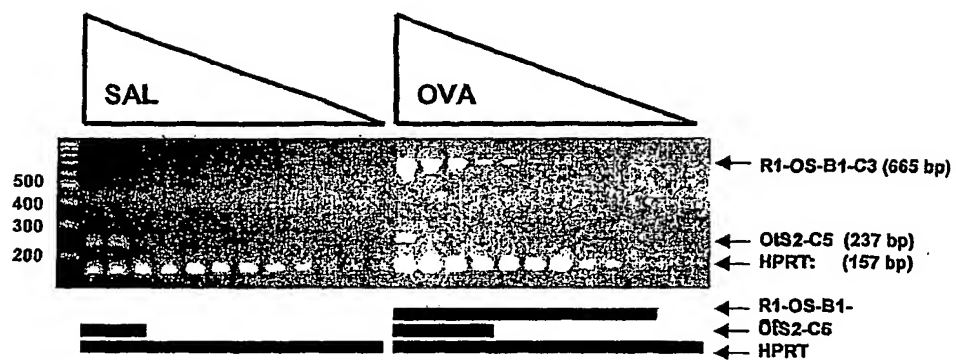
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nctctnnangggccca

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Figure 5A

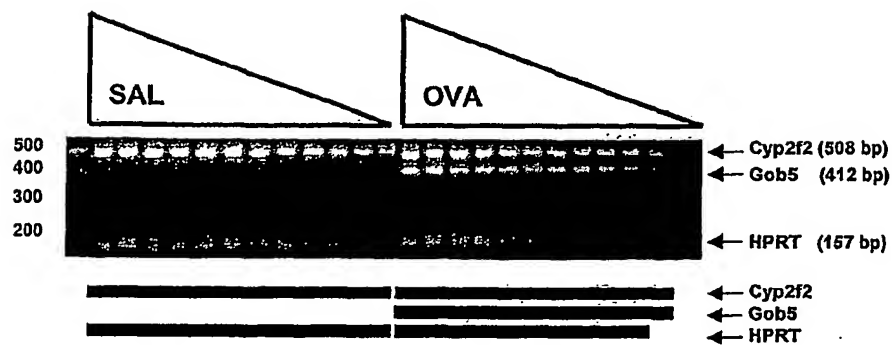


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Figure 5B

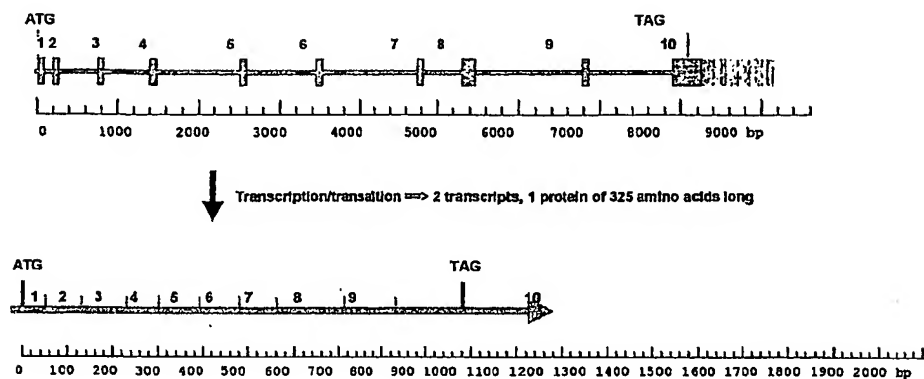


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Figure 6

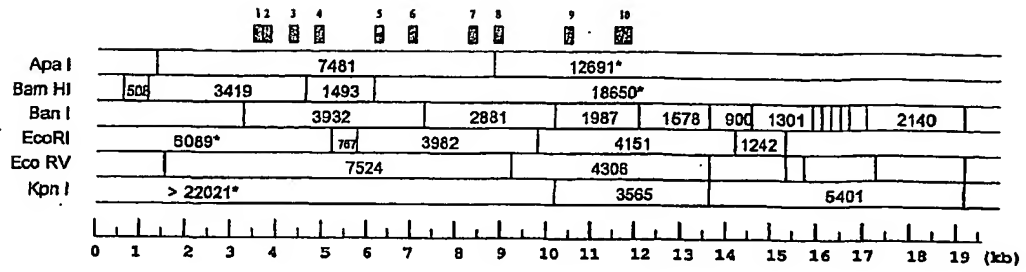


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Figure 7



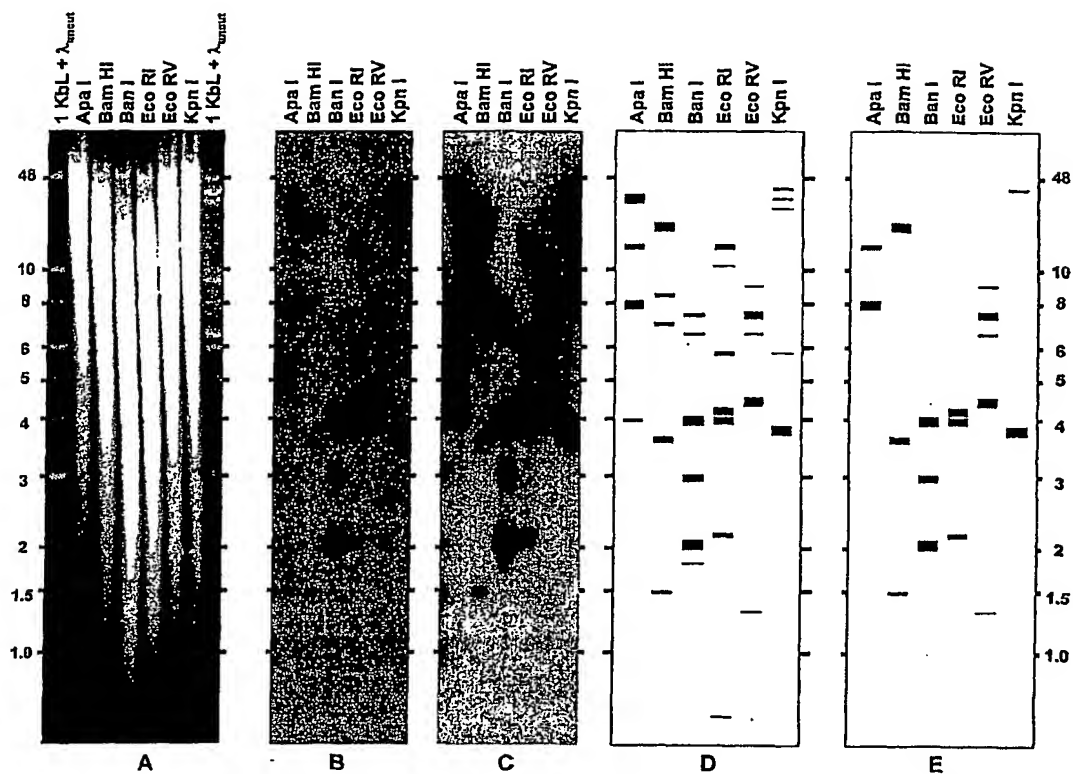


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Figure 8



Filter 180101A 2p127 Hybridisation 24/01/01 2p137 Probe: OtS1-B7-cDNA 47-51 = 1101 bp cDNA (+1: ATG; +978: TAG)  
A: EtBr; B, C: 2 and 5 day exposures; D: interpretation (predicted bands red); E: idem, only predicted bands

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Figure 9

BASE COUNT 6308 a 4234 c 4316 g 4761 t  
ORIGIN

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Figure 9, Contd.

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9421 taggagagaa tcaactctt aagatgccct ctgacagaca tacctgcact gtggcatatg
9481 cccatccaga catagaagta gacataatta taagaaaaaa tgaagtccctg acatgggtct
9541 gcttcacaag cttgaagacc ttgagttaa atccaaagat aaaggaggaat ggggtgagat
9601 ggctcagtag atgaaggcgc ttgtgccaa gcctgacaat ttatcctctg aacctacatg
9661 gttcagagaa ccaacccta taaattgtcc tttagacctc atgtacaggc atattaatat
9721 ccataagaca tatacataga taagcatgca taca cgcata acctgatag atattgaatt
9781 ctctgtgtgt aaatatctc accatgacag cttcaagttt ataatgggat gccactgaag
9841 aactgaaaag aaagggtatg tttcttaggt aacctgaat tagcatcatt tgcctctatc
9901 acattaaagc cagccatgag gaaattctat agactcattc tatagactca gaattcttaa
9961 gagccatcca gcaacattag cagaattggg gagggatgaa cagctgtgta attcgtgtgt

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Figure 9, Contd.

10021	gtgcgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt
10081	ttcagacagg	gtctcaactct	agttctatct	ggcctggaac	tcacagaaat	cctgtgggtt
10141	tctgagatta	aaggcatgta	cgtcatgtc	catgcagcta	ggtaccaccc	tatgccaagt
10201	gaatgtactg	ccataggcta	cagatgtaaa	aatagctgac	accatctaag	cacacatgag
10261	tactcatggc	ctgatatagc	ataaggggaa	aagataatgt	tgtaataga	agtttctgcc
10321	tgaggttggg	gagacaagct	gaaagtagga	aactctcccc	tgactgtcct	cctctttacc
10381	tccagacctt	cctgcagcag	acttctaagg	ctaaaggacc	aacctggatg	ggcctgtcag
10441	acctgaagaa	ggaggccacg	tggctctggg	tagatgggtc	tactctgtca	tccaggtaga
10501	tccagtgaac	aaccagtagt	gtagtccaga	caggctctctg	atgttctgat	agctacctgt
10561	gagtcctatc	ctctctctcc	tcacctctta	gaaataagag	ccaccatata	tagctgatgg
10621	aaggaagttt	tcctacccat	gcacagatag	aatatcagca	aatcccacca	tcaaagcaac
10681	aagaaaaact	tccccctgag	gggtgttaat	tttaattgtag	gctatttagta	gaaaatacaa
10741	aataaagtaa	ggccacaggg	taaggggact	attaacattg	aaagatatata	tattgggttg
10801	gggatataaa	tatgttcttt	aagttagcata	aggtttgatc	ccccattgca	atagtctgat
10861	atgggtgtcc	atgcctataa	caccagcagt	tggaggtag	agggagaaga	atcagttcaa
10921	tgttatcttc	agctacaaaa	tgggttctga	gacagcctga	gctacacagg	aagggaagggg
10981	gagagagaaa	gagaaaagca	ggtagggaag	gaaatgtaaa	gaaggggaag	aggacaacag
11041	tagcttaaa	ggagtttata	tggatgttca	ccgatccccc	agcacaacac	agagaacatg
11101	gggaagaacc	acaacaatc	agaataaaaa	ggaaggacac	actgtgggaa	agaaccttta
11161	ctttgttgtc	catgctaag	aacaggagag	actggcttgg	catctattag	tttaccatct
11221	taactttctg	atccctaatt	gtcttaacaa	tgttggcat	gtggcagatg	tattgtggac
11281	cagaatgcaa	gaaccagta	aggaaggcaa	aatccagatt	gattgtttaa	caccacaaaa
11341	ataaaataaa	ataaaataaa	ataaaataaa	ataaaataaa	ataaaataaa	ataaaataaa
11401	atagaaaaac	ccacaccact	ccttcaatgt	aggatataac	aagagtcatt	ttccaaagcc
11461	agcagaccca	ggcatgcccc	catctccaga	ggaaggccca	tctacaatat	gcattctgga
11521	aggaggtaaa	gacattgagt	ttcagaaaag	taaaaatatg	gcattgttca	cagcatgcca
11581	ctggagcaga	ctaactgttt	tctggctgac	tttccagatt	ccagaaatat	tggaaatagag
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11761	aaggctagct	catctctcgt	cctaccttca	tgccattctg	ccaggccacat	ggatgtgcct
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11881	ggattctctt	ttttatcaga	tttttcatcc	tctgcattta	tcattagtctt	atttctgttg
11941	atgtgataaa	actctctaac	caaaaacaac	taaggcagaa	aggggtttat	tttaccttac
12001	attccagatg	agagcaggga	ggtcaggatg	gcaggaaact	aagacaattg	gtcacatcac
12061	atcaaacagg	aggagagac	agaagtatgt	gcaagctaac	gcacacattt	gcttattctc
12121	agttccattt	tcctattcct	atagtcttag	acccctgccc	aggaaatggg	gccattcata
12181	gttggctaga	tgttcccacc	tctgttaact	tcaataagac	aagcccccc	agacatgctc
12241	actggccaac	ccaatgcagg	caatacacca	ttgagcctct	tcccagggtga	ctatacgtg
12301	tgtcaggctg	actatcacaa	agggactcac	tattgtcctt	ttgttttcag	gtttctctgg
12361	gcttagggct	cactgttgct	ccccacttcc	agtgcagtta	cctgatgtag	gatgctttca
12421	gaatctgggt	gttttccatt	aacctactcc	atcttccctg	ctgagacaca	tacactcaaa
12481	ggtcagaaga	agacattggt	gttctctttg	atagctcttt	actcccttga	gacaggagtt
12541	ggagttcatt	atttttttag	caaggctggg	gatctgaaag	atccaacatt	tttctgtctc
12601	cactcacctc	ctaaatgaag	ttacagtcac	atgtggccat	gtctggcctc	taacaattac
12661	tagggcttca	aggtcaggcc	ctctttcttg	cacatcagca	ctcttatcca	ctaagcatct
12721	ccccagccat	ttgtctattg	tcaggtagtc	tagtttactg	ttgtgttaat	aaagtcctga
12781	caaaatgcaa	gttggaagag	aaatggatta	tttgacttac	aattctagat	tgtagctcat
12841	ccctgcagga	atatcaagga	aggaaactga	atcagctcat	gatattacat	ccaaaagcag
12901	agagaataag	ttgcatgcat	gcctaatttt	tctaactgaa	tacagtcgcc	caactccaga
12961	gaatgggtgt	gccatattag	gatgggtttc	tgttcaattg	acttaagaca	atgaccccc
13021	ccatggatat	ttctgcaacc	tcgccccaaa	tagaccttat	tgaggatat	tcttctaggt
13081	tgtgtcaaac	tgggcaactaa	agctaaccat	cacatcaagt	cctatctgcc	tagtccccct
13141	agacttgatc	ctatctctgt	atactttcat	tctatctgtt	cacttacatc	aacctgctg
13201	aaaacttttg	gctaggaacc	ttccctggcc	tctgtagctc	atcatgcaaa	ctaagcatg
13261	aagatcatcc	ttcttctcca	tctatgactt	ccaggcatca	tcacacaaat	atttcagctc
13321	aggtgctgga	gaaacggctc	agcagtttaag	aatgcactca	ttgtctcctt	agaggagcat
13381	agctctcagc	aatcgtacct	gatgaaactc	cagctccagg	gaatctatca	cctttttatg

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Figure 9, Contd.

13441	gcttctgtgt	gcatttgaac	ttatgtgggg	tataaacaca	catcacaca	cattgtacat
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13561	ctggttccta	tcttggagat	atcatggtgg	atactgagag	ctccaagatt	tctcctcaga
13621	agagaatgtc	ttttccttct	attagacagt	attctattct	attccaattg	atctgtgggg
13681	tgtgtgtgt	gtgtgtgtgt	gtttgtgtgt	gtgcacgcgc	gcgtgcatgc	gcagtcacat
13741	acacagggtac	cacgatttat	tttttattac	tatggctggg	gcagaagtca	ctgagaccct
13801	tctttaagat	ccctatttag	aaactccata	atthtcccag	aaactatcca	taaagttggg
13861	tttccagcat	ctgacacaa	ctgttcaggc	ctttggctgt	gactgtttgt	ggctttgggt
13921	gtggctgtgg	ccgtggctgc	attcaactgaa	atatctatga	ccagtcctct	aagattgttg
13981	aaagccatat	ttagaatgta	gcttgtcaat	atgaccattt	atgaaaacag	cagtactaag
14041	tttctccag	gtgtatggcc	tcaccagctg	tggatttttg	gtcaaatttt	gtaccagtca
14101	tgaattcctt	cctaaagaga	aggcatcaat	acagtaagaa	atagttggac	actcccatat
14161	cagtcatgca	tcagtggaaa	catatttaat	aaagaaaata	caacacacaa	ccacttttcc
14221	aaacaacttt	tgctttattt	gtttttttta	aaagaaagcc	aatatttact	tttcatcttt
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14341	atgcctttta	tctcagctga	acatctcaac	ttcttgtcgt	tgtctcttca	tcttaacatc
14401	tgtatttcca	ctctcctctg	gacttaatat	ctgggtccac	aaactccact	aaaaattctg
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14581	acctggaacc	tcagagggca	tgccagttcc	cagaacccca	gaatttcaga	ggttagtcca
14641	catagggcac	caaaccactg	atggagacac	actactagac	ctgaagactt	attgggtcatc
14701	agaaccatag	gttactcaaa	ccagaagacc	agaaaggaaa	ccaaagcagt	gggaaaaaac
14761	atccaacaaa	gataaagtca	gcaatgatca	cctaaacata	taataaccaa	accagatga
14821	ctagaggcca	gcatatgaac	acagtcaaca	atatccaagg	caatacatca	ccaccagagc
14881	tatctctcta	cagaaagcac	tgaatttttt	taacacagct	gaagcacatg	aaaattacct
14941	taaatccaat	cttatgaaga	taatagagac	ctttaaagaa	gaaatacaaa	aaaaaaaaac
15001	cttaaaca	tcaggggtgag	agtaagggag	gcaaacagat	aaaggaatgt	gtttaagatg
15061	tgaaaataga	aatagacgaa	taaatgaaat	acaaactgat	ggaatactgg	aatggaaaa
15121	tctaggttaag	ttaacagaac	ctacagacag	aagtatcact	aacagaatac	aagagatgga
15181	aaaggatata	aggcatagaa	gataagatag	aagaaactaa	tatggcattt	aaaaatgtt
15241	atatctaaaa	aggctctgac	acaaaatgtt	caggaaatca	aggaaactat	aaagagacca
15301	aacctaaaga	caataggaat	agaagaggga	gatttccagc	tcagaattct	taggaaaaaa
15361	tacctaacct	aaagaagggtg	atgcctataa	aggtacaaga	aacatacaga	agaccataa
15421	tgttggacca	gaaaagaaag	tcttcccag	agataataat	caaaacacta	aatgtacaga
15481	gggaagaata	ttaaaagcta	aaagaggaaa	aggcacaaa	aaaaccaaca	acaacaacaa
15541	aaacatgtaa	aggcaaacct	agtagaatta	tgccctactt	ctcaacagaa	aatctaaaaa
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15661	cgactgtaac	aagcaaaact	ttcaatcacc	atagatggag	aaaacaagat	attctatgtc
15721	aaacccaat	ctaaatacga	tctttctatt	aatccagccc	tacagaggct	acaagaagga
15781	aaacttcgtt	ggtccgggac	ccgccgaact	taggaaattt	gtctgaacag	gtgagagggt
15841	gcgccagaga	acctgacagc	ttctggaaaca	ggcagaagca	cagaggcgct	gaggcagcac
15901	cctgtgtggg	ccggggacag	ccggccacct	tccggaccgg	aggacagggtg	ccacccggc
15961	aggggaggcg	gcctaagcca	cagcagcagc	ggtcgccatc	ttggtccggg	accgccgga
16021	cttaggaaat	tagtctgaac	aggtgagagg	gtgcgccaga	gaacctgaca	gcttctggaa
16081	caggcagaag	cacagaggcg	ctgaggcagc	accctgtgtg	ggccggggac	agccggccac
16141	cttccggacc	ggaggacagg	tgcccaccgg	gcaggggagg	cggcctaagc	caacagcaga
16201	gcggctcgcca	tcttgggtccg	ggaccgcggc	aacttaggaa	attagtctga	acagggtgaga
16261	gggtgcgccca	gagaacctga	cagcttctgg	aacaggcgga	agcacagagg	cgctgaggca
16321	gcacctgtg	tgggcccggg	acagccggcc	accttccgga	ccagaggaca	ggtgcccacc
16381	cggctgggga	ggcggcctaa	gccacagcag	cagcggctgc	catcttgggtc	cgggaccggc
16441	cgaacttagg	aaattagtct	gaacagggtga	gagggtgcac	cagagaacct	gacagcttct
16501	ggaacaggca	gaagcacaga	ggcgctgagg	cagcaccctg	tgtgggctgg	ggacagccgg
16561	ccaccttccg	gaccagagga	caggtgcccg	cccggtggg	gaggcgacct	aagccacagc
16621	agcagcggtc	gccatcttgg	tccgggaccc	gccgaactta	gggaattagt	ctgaacaggt
16681	gagagggtgc	gccagagaac	ctgacagctt	ctggaacagg	cgggaagcaca	gagggcgtga
16741	ggcagcacc	tttggggcc	ggggaacccc	agccaccgtc	cggaccggag	gacaggtgcc
16801	tgtccggctg	gggaggcggc	ctaagccaca	gcagcagcg	tgcctatctt	ggtccgagac

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Figure 9, Contd.

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16861 ccgccgaact taggaaatta gtctgaacag gtgagaggggt gcgccagaga acctgacagc
16921 ttctggaaca ggcagaagca cagaggcgct gaggcagcac cctgtgtggg ccggggacag
16981 ccggccacct tccggaccgg aggacagggtg cccacccggc aggggaggcg gcctaagcca
17041 cagcagcagc ggtcaccatc ttggtcccgg gactccaagg aacttaggaa ttagtcttgc
17101 ttagggtgaga gtctgtacca cctgggaact gccaaagcaa cacagtgtct gagaaaggctc
17161 ctgttttggg ccttcttctt cggccaggag gaggtccaaa tacaagatat ctgocgacct
17221 tccctgt aag agagcttgcc agcagagagt gctctgagca ctgaaactca gaggagagaa
17281 tctgtctccc aggtctgctg atagacggta acagaatcac cagaagaaca atctctaaac
17341 agagtcaact ataactacta actccagaga ttaccagatg gcgaaaggta aacggaggaa
17401 tcttactaac aggaaccaag accactcacc atcaccagaa cccagcacac ccacttcgcc
17461 cagtccaggg aacccaaca cacctgagaa cctagaccta gat ttaaaag catatctcat
17521 gatgatggta gaggacatca agaaggactt taataaatca cttaaagaaa tacaggagaa
17581 cactgctaaa gaggtaacaag tccttaaga aaaaaggaa aacacaatca aacaggtaga
17641 agtccttaca gaaaaagagg aaaaacata caaacagggtg atggaaaatg aacaaaacca
17701 tactagacct aaaaagggaa gtagacacaa taagaaaaac tcaagcgag gcaacgctag
17761 agataga aac cctaggaaag aaatctggaa ccatagattt gagcatcagc aacagaatac
17821 aagagatgga agagagaatc tcaggtgcag aagattccat agagaacatc ggcacaacaa
17881 tcaagaaaaa tggaaaatgc aaaaagatcc taactcaaaa tatacaggaa atccaggaca
17941 caataagaag accaaaagta cggataatag gaggatga gaatgaagat tttcaactca
18001 aagggtccagc aaacatcttc aacaaaatta ttgaagaaaa cttcccaaat ct aaagaatg
18061 agatgcatat gaacatacaa gaagcctaca gaactccaaa tagactggac cagaaaagaa
18121 attcctcccg acacataata atcagaacat caaatgcact aataaagat agaatactaa
18181 aagcagtaag ggaaaaagggt caagtaacat ataaaggcaa gcctatcaga at tacaccag
18241 atttttacc agagactatg aaagccagaa gagcctggac agatgttata cagacactaa
18301 gagaacacaa actgcagccc aggtactat atccagccaa actctcaatt at catagagg
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18421 cccttca aag gataataaca gaaaaaaacc aatacaagaa cgggaacaac gccctagaaa
18481 aaacaagaag gtaatccttc aacaaaccta aaagaagaca gccacaagaa cagaatgccca
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18601 aatgggtctca actcgccaat aaaaagacat agactaacaa ctggctacac aaacaagacc
18661 caacattttg ctgcttacag gaaactcatc tcagagaaaa agatagacac tacctcagaa
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Figure 10

1	MSDSTEAKMQ	PLSSMDDDEL	MVSGSRYSIK	SSRLRPNSGI	KCLAGCSGHS	QVPLVLQLLS	60
61	FLFLAGLLLI	ILFQVSKTPN	TERQKEQEKI	LQELTQLTDE	LTSRIPISQG	KNESMQAKIT	120
121	EQLMQLKTEL	LSRIPIFQGQ	NESIQEKISE	QLMQLKAELL	SKISSFVKD	DSKQEKIYQQ	180
181	LVQMKTLEFR	LCRLCPWDWT	FLLGNCYFFS	KSQRNWDAV	TACKEVKAQL	VIINSDEEQT	240
241	FLQQTSKAKG	PTWMGLSDLK	KEATWLWVDG	STLSSRFQKY	WNRGEPNNIG	EEDCVEFAGD	300
301	GWNSDKCELK	KFWICKKSAT	PCTEG				325



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Figure 11

Sequence format is Pearson

Sequence 1: AAF77072 404 aa

Sequence 2: OtB7-ORF 325 aa

Sequences (1:2) Aligned Score: 45

```

AAF77072      MSDSKEPRLQQQLGLLEEEQLRGLG-----FRQTRGYKSLAGCLGHG--PLVLQLLS 49
OtB7-ORF      MSDSTEAKMQPLSSMDDDELMVSGSRYSIKSSRLRPNSGIKCLAGCSGHSQVPLVLQLLS 60
              ****.*.:.* *. :.:.* * : * . * *.***** *. *****

AAF77072      FTLLAG---LLVQVSKVPSSISQEQSRQDAIYQNLTLKAAVGESEKSKLQEIYQELT 105
OtB7-ORF      FLFLAGLLLIILFQVSKTPN--TERQKEQEKIQLQELTQLT---DELTSR----- 104
              * :*** :*.*****. :.:.*.: * *:*****. .*:.:

AAF77072      QLKAAVGEPEKSKLQEIYQELTRLKAAVGEPEKSKLQEIYQELTWLKAAVGEPEKSK 165
OtB7-ORF      ---IPISQGNESMQAKITEQLMQLKTEL----- 130
              .:.: :.* :* :.* :*: :

AAF77072      MQEIYQELTRLKAAVGEPEKSKQOEIYQELTRLKAAVGEPEKSKQOEIYQELTRLKAA 225
OtB7-ORF      -----LSRIPIFQGN--ESIQEKISEQLMQLKAE--LSKISSFP----- 167
              *: *: * : * : * : * : * : * : * : * : * : * :

AAF77072      VGELPEKSKQOEIYQELTQLKAAVERLCHPCPWEWTFQGNCFMSNSQRNWHD SITACK 285
OtB7-ORF      ---VKDDSKQEKIYQQLVQMKTFLRLCRLCPWDWTFLLGNCYFFSKSQRNWDAVTACK 224
              : :.***:***:*.***: : ***: ***:***: *****:*****:*.***

AAF77072      EVGAQLVVIKSAAEQNFLQLQSSRSNRFTWMGLSDLNQEGTWQWVDGSPLLPSFKQYWNR 345
OtB7-ORF      EVKAQLVIINSDEEQTFLLQ-QTSKAKGPTWMGLSDLKKEATWLWVDGSTLSSRFQYWNR 283
              ** *****:.* ***.*** *: : : *****:*.** *****. * . *:*****

AAF77072      GEPNNVGEEDECAEFSGNGWNDDKCNLAKFWICKKSAASC SRDEEQFLSPAPATPNPPPA 404
OtB7-ORF      GEPNNIGEEDCVEFAGDGWNDSKCELKKFWICKSATPCTEG----- 325
              *****:*****.***:*.*****.***: * *****:*.***

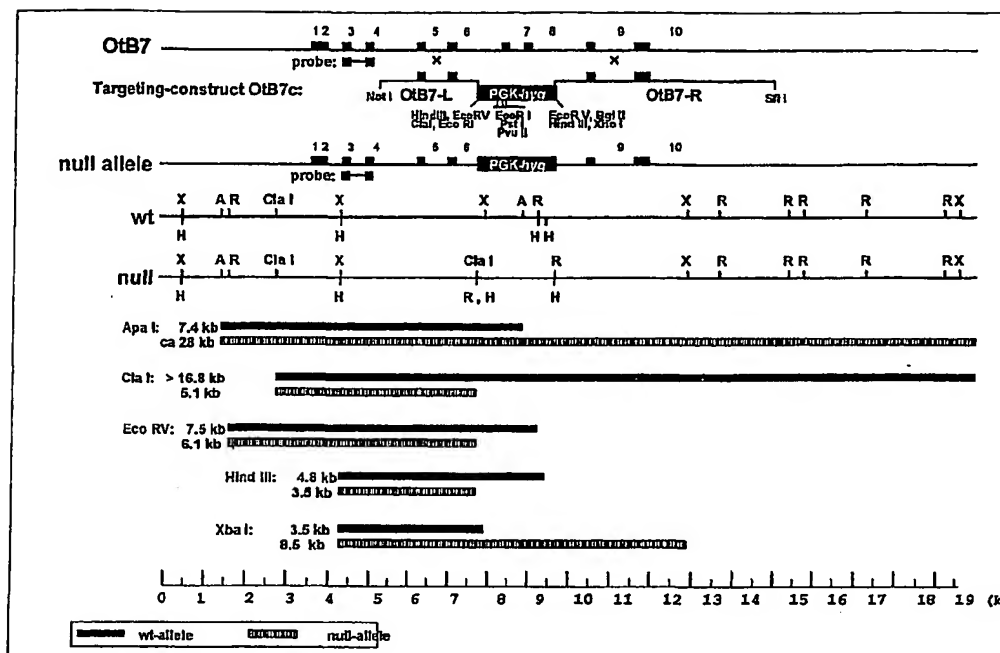
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Figure 12

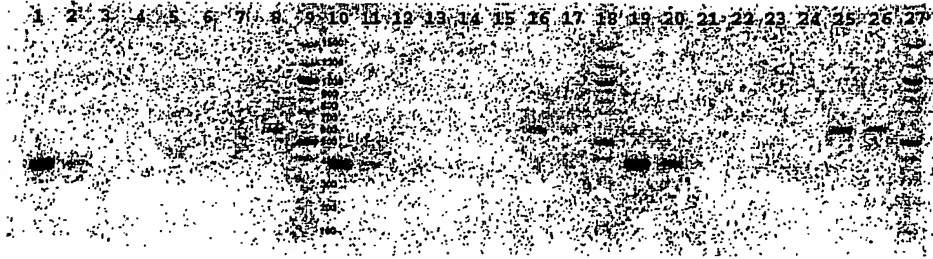


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Inventor: Grout et al.  
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Figure 13



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FIGURE 14

Gob-5 --MBSLKSPVFLLIHLLHLEGALNSL-----IQLNNNGYEGIVIAIDHDPVPEDEALIQH 52  
HuCLCA1 --MGPFKSSVFLIILHLLLEGALNSL-----IQLNNNGYEGIVVADPNVPDETLIQH 52  
HuCLCA4 --MGLRFGVFLVLICLLH-QSNTSF-----IKLNNNGFEDIVVIDPSPVEDKILIQ 51  
MuCaCC --MVPGLQVLLFLTLHLHQ-NTSSM-----VHLNSNGYEGVVIAINPSVPEDRLIPS 51  
HuCLCA2 MTQQRSTAGPICNLKFPVTLVALSSSELPFLGAGVQLQDNGYNGLLIAINPQVPEQNQLISN 60  
: \* : \* : \*

Gob-5 IKDMVTQASPYLFEATGKRIFYFNVAII PESWIAKPEYTRPKLETFNADVLVSTTSPL 112  
HuCLCA1 IKDMVTQASLYLFEATGKRIFYFNVAII PETWTKKADYVRPKLETYKNADVLVAESTPP 112  
HuCLCA4 IEDMTTASTYLETKRFFPKNVSILIPENWKNPQYKRPHENHKAADVIVAPPTLP 111  
MuCaCC IKBMVQASTYLEPEASQGRVYFRNISILVPMPTWRSKPEYLMPKRESYDKADVIVADPHLQ 111  
HuCLCA2 IKEMITEASFYLFNATKRRVFRFNRIKILPATWKAN--NNSKIKQESYEKANVITVDWYGA 119  
\* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Gob-5 GNDEPYTEHIGPCCEKGIIRIHLTPDFLAGKCLTQ-YGPDORTFVHEWAHFRWGVFNEYNN 171  
HuCLCA1 GNDEPYTEQMGCCEKGERIHLTPDFLAGKCLAE-YGPGKAFVHEWAHLRWGVFDEYNN 171  
HuCLCA4 GRDEPYTKQFTECEKGEYIHTFPDLLLGKKQNE-YGPPGKLFVHEWAHLRWGVFDEYNE 170  
MuCaCC HGDDPYTLQYGCCEDRGQYIHTFPNLLTDLNLR-YGPRGRVVFHEWAHLRWGVFDEYNV 170  
HuCLCA2 HGDDPYTLQYRCCEKKGKGIHTFPNLLNDNLTAGYGSRGVVFHEWAHLRWGVFDEYNN 179  
\* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Gob-5 DEKFYLSKGGK-PQAVFCSAAITGKNQVRKCGGSGCTGKCVIDRVTLGLYKONCVFVDP 230  
HuCLCA1 DEKFYLSNGR-IQAVFCASAGITGTNVVKCGGSGCTK-RCTFNKVTGLYEKGCBFVLQS 229  
HuCLCA4 DQPFYRAKSKIEATFCASAGISGRNRVYKCGGSGCLSR-ACRIDSTTKLYGKDCQFFPDK 229  
MuCaCC DQPFYNSRIKNTIEATFCSTRITGTNVVHCEGRNCVTR-ACRDSKTRLYEPKCTFIPDK 229  
HuCLCA2 DKPFYINGQNIKVTETCSIDITG---IFVCEKGECPQE-MCIIIS---KLFKEGCTFIPYS 232  
\* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Gob-5 HQNEKASIMFNQINNSVVEFCTEKNHMQEAPNDQNQRCNLRSTWEVIQESDFKQTTPM- 289  
HuCLCA1 RQTEKASIMFAQHVDISIVEFCTEQNHKNKAPNKNQKCNLRSTWEVIRDSEDFKTTTPM- 288  
HuCLCA4 VQTEKASIMFMQSDISVVEFCTEKNETHNQEAPLNQIKCNFRSTWEVINSDFKNTTIPM- 289  
McCaCC IQTAGASIMFQNLNSVVEFCTEKNHNAEAPNLQKNMKNRRSTWDVITKTSADFNQAPMR 288  
HuCLCA2 TQNATASIMFMQSLSSVVEFCNASTHMQEAPNLQNMCMCLSRSAWDVITDSADPHSFPMN 292  
\* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Gob-5 -TAQPPNPTFSLLOIGORIVCLVLDKSSGSLNDDRLNEMNQASRLFLLQTVEQGSWVG 348  
HuCLCA1 -TTQPPNPTFSLLOIGORIVCLVLDKSSGSLATGNRLNRLNQAGQLFLLQTVEQGSWVG 347  
HuCLCA4 -VTPPPPVFSLLKIRQIVCLVLDKSSGSGGKDLNRLNMQAAKHLFLLQTVEQGSWVG 347  
McCaCC GTEAPPPPTFSLLSRRRVCLVLDKSSGSHDKEDRLNMQAAELYLTLQIVEKESMVG 349  
HuCLCA2 GTELPNPTFSLVQAGDKVCLVLDVSSKMAEADRLQLQQAALFYLMQIVIEHTFVGIA 352  
\* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Gob-5 TFDASAAYQSELEQLNSGADRDLILKHLPTVSAGGT--SICSGLRFTAFTVIKKKYP-TDG 405  
HuCLCA1 TFDASAAYQSELIQNSGDRDLTAKRLPAASAGGT--SICSGLRFTAFTVIKKKYP-TDG 404  
HuCLCA4 HFDSTATIVNKLIQIKSSDERNTLMAGLPTYPGGT--SICSGIKYAFQVIGELHSLQDG 405  
McCaCC TFDASAHIQNTYLKIKTSSSDYQKITANLPPQASAGGT--SICHLQAGFAITSSDQSTG 407  
HuCLCA2 SFDSEKIEIRAQLHQINSNDDRLKLVSLPTTVAKTDISICSGLKGKGFVEVKEKNGKAY 412  
\* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Gob-5 SEIVLLTDGEDNTISSCFDLVKQSGAIHTHTVALGPSAAQLELSELSKMTGGGLQTTASDQVQ 465  
HuCLCA1 SEIVLLTDGEDNTISSCFNEVEKQSGAIHTHTVALGPSAAQLELSELSKMTGGGLQTTASDQVQ 464  
HuCLCA4 SEIVLLTDGEDNTASSCIDEVKQSGAIFTIALGRAADEAVTEMSKITGGSFYFVSDQAE 465  
McCaCC SEIVLLTDGEDNGIESCFEAVERSGAIHTHTALGPSAAELETSRLTGGGLFYFVANKDLN 467  
HuCLCA2 SVMILVTSODDKLLKNCPLFTVLSSGSTHISIALGSSAAPNLELSRLTGGGLFFVFDISN 472  
\* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Gob-5 NNGLVDAFAALSSGNAAIAQHSIQLESRGVNLQNNQWMNGSVIVDSSVKGDTLFLITWTT 525  
HuCLCA1 NNGLIDAFGALSSNGCAVQSRHSIQLESKGLTLQNSQWMNGTVIDSTVGKDTLFLITWTT 524  
HuCLCA4 NNGLIDAFGALSGMNTDLSQKSLQLESKGLTLQNSNAWMNDTVIIDSTVGKDTLFLITWTT 525  
McCaCC --SLIDAFSRISSSTSGSVSQALQLESKAPDVRAGAWINGTVPDSTVGNDTFPVITWNV 525  
HuCLCA2 SNSMIDAFSRISSSGTGDIFQQHILQLESTGENVKPHHQLKNTVTVNDTGVNDTMFLVWQA 532  
: : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

Gob-5 H-PPTFIWDPSPGV--EQNGFILDIT-TKVAYLQVPGTAKVGFWKYSIQASS---QTLTL 578  
HuCLCA1 Q-PPQILLWDPSPGQ--KGGGFVVDKN-TKMYALQIPGIAKVGTWYKYSIQASS---QTLTL 577  
HuCLCA4 L-PPSILWDPSPGT--IKENFTVADT-SKMAYLIPGTAKVGTWYNYLQAKAN-PETTL 580  
McCaCC K-KPRIILQDPKKGKYYTSDQDDKLNIRASRLQIPGTAARTGTWYISITGTKS---QLITM 582  
HuCLCA2 SGPPRIILPDPDGRKYTNNTNITLNT-PRTASLWIPGTAKPGHWTYTLNNTHTSHLQALKV 591  
\* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \* : \*

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FIGURE 14, CONTD.

```
Gob-5      TVTSRAASATLPPITVTPVVKNTGKFPSPVTVYASIRQGASPILRASVTALIESVNGKT 638
HuCLCA1    TVTSRASNATLPPITVTSKNTKDTSKFPSPVTVYANIRQGASPILRASVTALIESVNGKT 637
HuCLCA4    TVTSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHT 640
McACC      TVTTRARSPTMEPLLATAHMSQSTAQYPSRMIVYARVVSQGFLPVLGANVTALIEAEHG HQ 642
HuCLCA2    TVTSRASNSAVPPATVEAFVERDSLHFPHPVMIYANVKQGFYPILNATVTATVEPETGDP 651
          ***:*** . . . : * . . . : . : * : : ** : * * * : * . * . * .

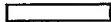
Gob-5      VTLELLDNGAGADATKNDGVYSRFFTAFDANGRYSVKIWALGGVTSRDRQRAAPPKNRAMY 698
HuCLCA1    VTLELLDNGAGADATKDDGVYSRYFTTYDTNGRYSVKVRALGGVNAARRRVIPOQSGALY 697
HuCLCA4    EVLELLDNGAGADSFKNDGVYSRYFTAYTENGYSYLVKVRHGGANTARLKLRPPLNRAAY 700
McACC      VTLELDWNGAGADTVKNDGIYTRYFTDYHGNSRYSYLVKVRVQAQRNKTLSLR-QKNKSLY 701
HuCLCA2    VTLRLDDGAGADVIKNDGIYSRYFFSFAANGRYSYLVKRVHNSPSTPAHSIPGSHAMY 711
          . . . * : * * * * * : * * * : * : * : * * * : * . * . * .


Gob-5      IDGWIEDGEVRMNP RP RP PETS--YVQKQKLCFSRTSSGGSEFVATNVPAAAPIPDLFPQCQI 756
HuCLCA1    IPGWIEWDEIQWNP RP PEINKDDVQHKQVCFSRTSSGGSEFVSDVFN-APIPDLFPQCQI 756
HuCLCA4    IPGWVVGGEIEANP RP PEYD-EDTQTLEDFSRASGGAFVVSQVPS-LPLPQYPPSQI 758
McACC      IPGYVENGKIVLNP RP PDVQEEAIEATVEDFNRTVSGGSFTVSGAPPDGDHARVFPFSKV 761
HuCLCA2    VPGYTANGNIQMNA PRKSVG-RNEEERKNGFSRVSSGGSFVGLGVPA-GPHPDVFPFCKI 769
          : : : . . . : * . * . : . : * . : * * * : * . * . * .

Gob-5      TDLKASIQGQNLVNLWTAPGDDYDHGRASNYIIRMSTSIVDLRDHFNLSLQVNTTGLIP 816
HuCLCA1    TDLNAEIHGGSLINLTWTAPGDDYDHGTAHKYIIRISTSILOLRDKFNESLQVNTTALIP 816
HuCLCA4    TDLDATVHEDKII-LTWTAPGDNFDVGKVRQYIIRISASILDLRDSFDDALQVNTTDLSP 817
McACC      TDLEAEFIG-DYIHLTWTAPGKVLNDRGHRHYIIRMSQHPDLQEDFNATLVNAGSLIP 820
HuCLCA2    IDLEAVKVEEELT-LSWTAPGEDFDQGGQATSYEIRMSKSLQNIQDDFNAILVNTSKRNP 828
          . . . * : * * * * * . * * . * * : * : * : * : * : * .

Gob-5      KEASSEEIFEFELGGNTFG-----NGTDIFIAIQAVDKSNLKSEISNIARVSVFI 866
HuCLCA1    KEANSEEVFLFKPENITFE-----NGTDLFIAIQAVDKVDLKSEISNIARVSLEFI 866
HuCLCA4    KEANSKESFAFKPENISEE-----NATHIFIAIKSIDKSNLTSKVSNIQVTLFI 867
McACC      KEAGSKETFKFKPETFKIA-----NGIQLYIAIQADNEASITSEVSNIAQAVKLT 870
HuCLCA2    QQAGIREIFTTFSPQISTNGPEHQPNGETHESHRIYVAIRAMDRNSLQSAVSNIAQAPLFI 888
          : * . . * * * . . : . : * * * : . . * * : * * * : .

Gob-5      PAQEP---PIPEDSTPPCPDISINS--TIPGIHVLKIMWKWLGEMQVTLGLH----- 913
HuCLCA1    PPQTTPPETPSPDETSAPCPNIHINS--TIPGIHLKIMWKWIGELQLSIA----- 914
HuCLCA4    PQANP-DDIDPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI----- 917
McACC      SLEDS-----ISALGDISAICMTIWLGLTVIFNSILN----- 901
HuCLCA2    PPNSD----PVPARDYLILKGVLTAMGLIGIICLIIVVTHHTLSRKKRADKKENGTKLL 943
          . . : * * : . .
```

 Conserved cysteines  
VWLTGGEN von Willebrand factor type A domain

 gn1|Smart|smart00322, VWA, von Willebrand factor (vWF) type A domain; VWA domains in extracellular eukaryotic proteins mediate adhesion via metal ion-dependent adhesion sites (MIDAS). Intracellular VWA domains and homologues in prokaryotes have recently been identified. The proposed VWA domains in integrin beta subunits have recently been substantiated using sequence-based methods (Ponting et al. Adv Prot Chem (2000) 54:185-244).

 MIDAS motif

Affinity regulation: MIDAS Bonds in CD11's

The metal ion-dependent adhesion site (MIDAS) is believed to be the site on the alpha chain of LFA-1 (alpha-L, CD11a) which binds ligand (ICAM-1, ICAM-2, or ICAM-3). Although it is likely to be a critical portion of the ligand-binding site, other parts of LFA-1 may also make important contributions, notably the MIDAS site on CD18, and the 4th and 5th repeats of CD11a. The MIDAS motif consists of DxSxS...T...D, and is equally central to ligand binding for both CD11a/CD18 (LFA-1) and CD11b/CD18 (Complement receptor type 3, CR3).

Forward primer

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FIGURE 15

```
BE655906      AGTCACTGGCGATCTGAAAAGTGTCTAGAGCAGGATCTAGCTGACTCTAAGATTGCAGGG 60
OtS2-D10      -----GATCTAGCTGACTCTAAGATTGCAGGG 27
CD59          AGTCACTGGCGATCTGAAAAGTGTCTAGAGCAGGATCTAGCTGACTCTAAGATTGCAG-- 63
               .....*****

BE655906      TTGAAGGTGTCTGTGAAGCCTGTGGAACTGCTGCTTTAAATCTTCAATCTGGCTGGG 120
OtS2-D10      TTGAAGGTGTCTGTGAAGCCTGTGGAACTGCTGCTTTAAATCTTCAATCTGGCTGGG 87
CD59          -----

BE655906      GATGTGGCTCAAGATAGTGTGCTGATGGTGGCCTGGCTTGGTTCTTCATATATTAAAAAT 180
OtS2-D10      GATGTGGCTCAAGATAGTGTGCTGATGGTGGCCTGGCTTGGTTCTTCATATATTAAAAAT 147
CD59          -----AT 65
               **

BE655906      TTGGTAGCCAGCACCAATGAGAGCTCAGAGGGGACTCATCTTACTCCTGCTGCTTCTGGC 240
OtS2-D10      TTGGTAGCCAGCACCAATGAGAGCTCAGAGGGGACTCATCTTACTCCTGCTGCTTCTGGC 207
CD59          TTGGTAGCCAGCACCAATGAGAGCTCAGAGGGGACTCATCTTACTCCTGCTGCTTCTGGC 125
               *****

BE655906      TGTGTTCTGTTCACAGCTGTTAGCCTCACATGCTACCACTGTTTCCAACCGGTGGTTTC 300
OtS2-D10      TGTGTTCTGTTCACAGCTGTTAGCCTCACATGCTACCACTGTTTCCAACCGGTGGTTTC 267
CD59          TGTGTTCTGTTCACAGCTGTTAGCCTCACATGCTACCACTGTTTCCAACCGGTGGTTTC 185
               *****

BE655906      TTCATGCAATATGAACAGCACTTGCTCTCCTGACCAGGATTCCTGTCTCTATGCTGTAGC 360
OtS2-D10      TTCATGCAATATGAACAGCACTTGCTCTCCTGACCAGGATTCCTGTCTCTATGCTGTAGC 327
CD59          TTCATGCAATATGAACAGCACTTGCTCTCCTGACCAGGATTCCTGTCTCTATGCTGTAGC 245
               *****

               <-----
               reverse

BE655906      CGGAATGCAAGTGTATCAAAGGTGTGGAAACAATCAGATTGTCATG----- 407
OtS2-D10      CGGAATGCAAGTGTATCAAAGGTGTGGAAACAATCAGATTGTCATGGTGATC----- 378
CD59          CGGAATGCAAGTGTATCAAAGGTGTGGAAACAATCAGATTGTCATGGTGAGATCATTAT 305
               *****
               -----
               primer
```

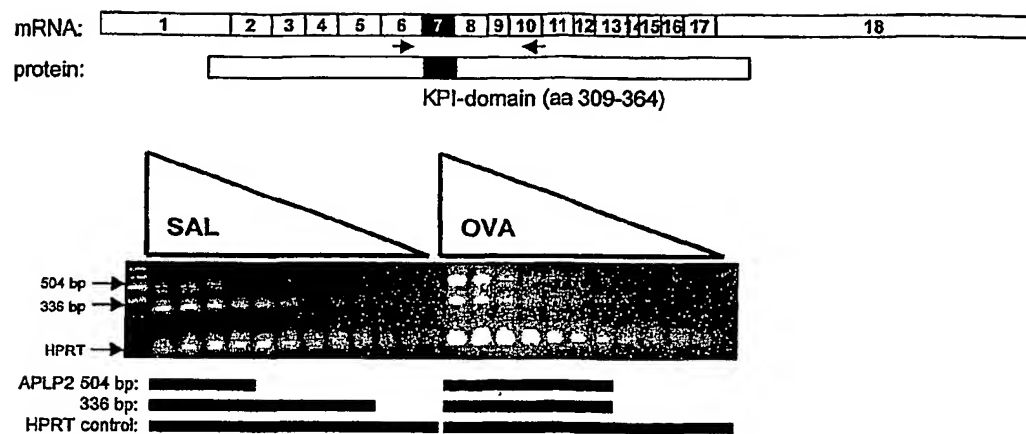
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Figure 16

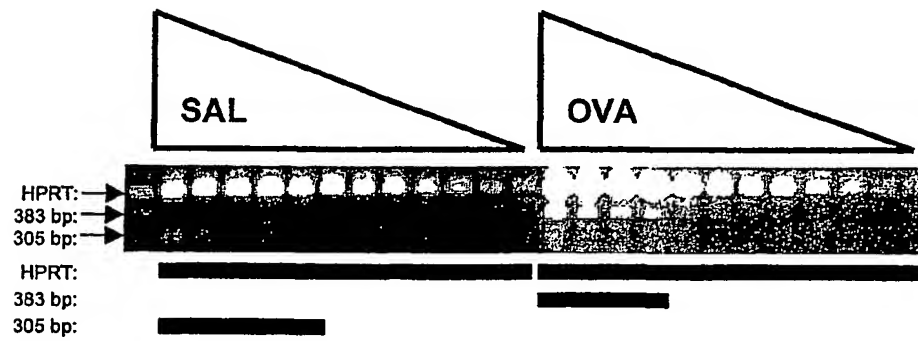


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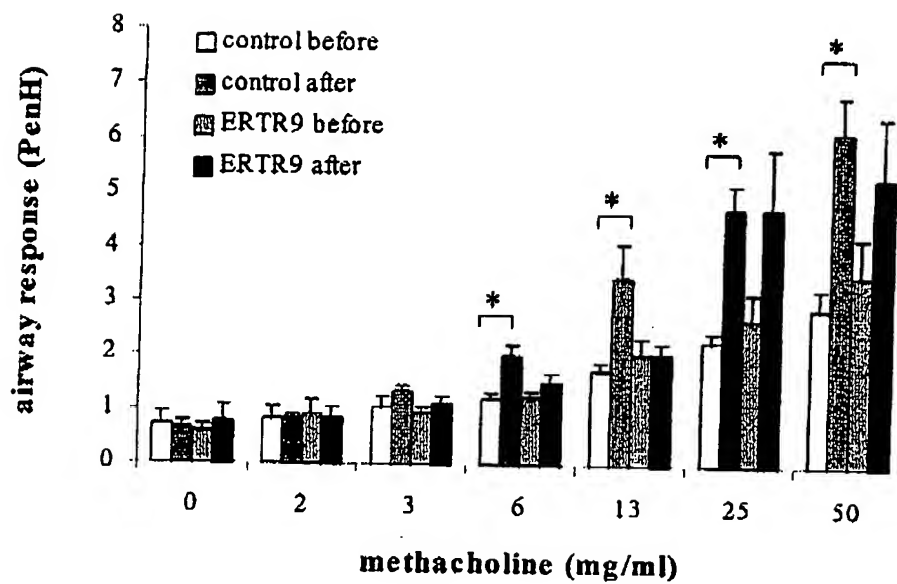
Figure 17





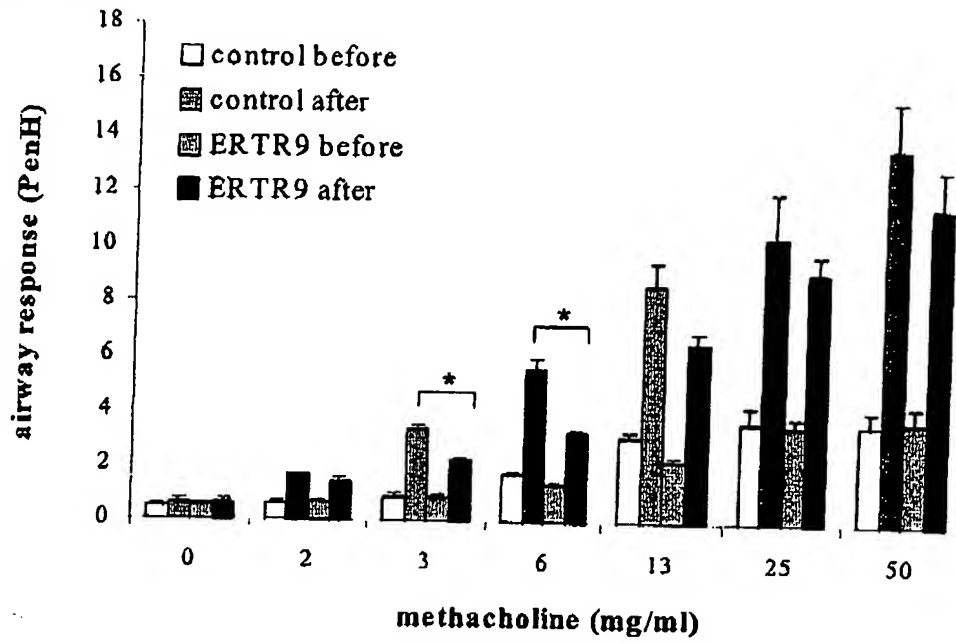
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Fig. 18A



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Fig. 18B



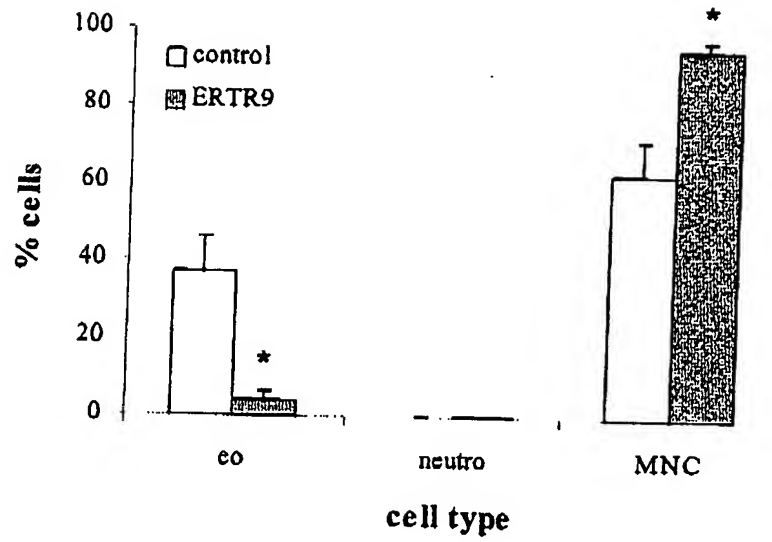
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Fig. 19A



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Fig. 19B

